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# from Ito and Houston (2004)
Calculate_Hepatic_Clearance <- function(Params)
{
  CLint <- get_param("CLint",Params,"Calculate_Hepatic_Clearance")
  fub <- get_param("fub",Params,"Calculate_Hepatic_Clearance")
  Qh <- get_param("Qh",Params,"Calculate_Hepatic_Clearance",default=20.7)
  CLint.scaling <- get_param("CLint.scaling",Params,"Calculate_Hepatic_Clearance",default=110)
  Dn <- get_param("Dn",Params,"Calculate_Hepatic_Clearance",default=0.17)
  density <- get_param("density",Params,"Calculate_Hepatic_Clearance",default=1.05)
  model <- get_param("model",Params,"Calculate_Hepatic_Clearance",default="well-stirred")

  if (!(model %in% c("well-stirred","parallel tube","dispersion")))
    stop("Model other than \"well-stirred,\" \"parallel tube,\" or \"dispersion\" specified.")

  # Convert from uL/min/10^6 cells to uL/min/g liver
  CLint <- CLint*CLint.scaling

  if (model == "well-stirred")
    CLh <- Qh*fub*CLint/(Qh+fub*CLint)
  else if (model == "parallel tube")
    CLh <- Qh*(1-exp(-fub*CLint/Qh))
  else if (model == "dispersion")
  {
    Rn <- fub*CLint/Qh
    a <- sqrt(1 + 4*Rn*Dn)
    CLh <- Qh*(1 - 4*a/((1+a)^2*exp((a-1)/2/Dn)-(1-a)^2*exp(-(a+1)/2/Dn)))
  }

  return(CLh)
}

```